IN THE CLAIMS

Please amend the claims as follows.

In Claim 57, fourth line, delete "insert" and substitute –insert.-- therefor.

23. The method of Claim 1 or 2 wherein said [first] nucleic acid [concentration] B1 fragment is present at [comprises] 10^{-21} to 10^{-14} mole [nucleic acid fragment per 1 to 10,000 microliters].

37. A linearized vector comprising an origin of replication, an insertion site, and B2 two complementary cohesive circularization ends, wherein:

each of said cohesive circularization ends is at least about 20 base pairs from said insertion site;

said cohesive circularization ends are between about 8 and about 50 nucleotides in length; and

upon hybridization of said cohesive circularization ends, said cohesive circularization ends cannot be [ligase does not] substantially covalently joined by ligase [join said cohesive circularization ends].

54. A linear nucleic acid insert-vector construct with complementary cohesive B3 circularization ends, wherein said cohesive circularization ends (1) are between about 8 and about 50 nucleotides in length, (2) are at least about 20 base pairs from each end of said nucleic acid insert, and (3) upon hybridization of said cohesive circularization ends, said cohesive circularization ends cannot be [are not] substantially covalently joined by ligase.

60. A genomic or cDNA library in a linear vector with complementary cohesive B4 circularization ends, wherein said cohesive circularization ends (1) are between about 8 and about 50 nucleotides in length, (2) are at least about 20 base pairs from each end of a genomic